

SEQUENCE LISTING

<110> Presnell, Scott R.
 Xu, Wenfeng
 Kindsvogel, Wayne
 Chen, Zhi

<120> Human Cytokine Receptor

<130> 99-93

<150> US 60/169,049

<151> 1999-12-03

<150> US 60/232,219

<151> 2000-09-13

<150> US 60/244,610

<151> 2000-10-31

<160> 36

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2149

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(693)

<400> 1

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Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu	
1 5 10 15	
act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag	96
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln	
20 25 30	

agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag	144
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln	
35 40 45	
cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac	192
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr	
50 55 60	
aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt	240
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly	
65 70 75 80	
act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag	288
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln	
85 90 95	
gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca	336
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser	
100 105 110	
gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata	384
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile	
115 120 125	
gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta	432
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val	
130 135 140	
att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat	480
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn	
145 150 155 160	
gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att	528
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile	
165 170 175	
aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga	576
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg	
180 185 190	
gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg	624
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val	
195 200 205	

gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa 672
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

gag aga tgt gtg gaa att cca tgacttgtgg aatttggcat tcagcaatgt 723
 Glu Arg Cys Val Glu Ile Pro
 225 230

ggaaattcta aagctccctg agaacaggat gactcgtggt tgaaggatct tatttaaaat 783
 tgtttttgta ttttcttaaa gcaatattca ctgttacacc ttggggactt ctttgtttat 843
 ccattctttt atcctttata tttcatttta aactatattt gaacgacatt ccccccgaag 903
 aattgaaatg taaagatgag gcagagaata aagtgttcta tgaaattcag aactttattt 963
 ctgaatgtaa catccctaata aacaaccttc atttcttcta tacagcaaaa taaaaattta 1023
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 caacagaaag ctgccttctt cacttgaggc taagtcttca tatatgttta aggttgtctt 1863
 tctagtgagg agatacatat cagagaacat ttgtacaatt ccccatgaaa attgctccaa 1923
 agttgataac aatatagtcg gtgcttctag ttatatgcaa gtactcagt ataaatggat 1983
 taaaaaatat tcagaaatgt attgggggt ggaggagaat aagaggcaga gcaagagcta 2043
 gagaattggt ttccttgctt ccctgtatgc tcagaaaaca ttgatttgag catagacgca 2103
 gagactgaaa aaaaaaaaaat gctcgagcgg ccgcatatc cttggt 2149

<210> 2

<211> 231

<212> PRT

<213> Homo sapiens

<400> 2

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 20 25 30
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220
 Glu Arg Cys Val Glu Ile Pro
 225 230

<210> 3

<211> 693

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:2.

<221> misc_feature

<222> (1)...(693)

<223> n = A,T,C or G

<400> 3

atgatgccna arcaytgytt yytnggntty ytnathwsnt tyttyytnac ngngngtngcn 60
 ggnacncarw snacncayga rwsnythaar ccncarmgng tncarttyca rwsnmgnaay 120
 ttycayaaya thytncartg gcarccnggn mgngchnytna cnggnaayws nwsngtntay 180
 ttygtncart ayaarathta yggncarmgn cartggaara ayaargarga ytgytggggg 240
 acncargary tnwsntgyga yytnacnwsn garacnwsng ayathcarga rccntaytay 300
 ggnmgngtnm gngcngcnws ngcnggnwsn taywsngart ggwsnatgac nccnmgntty 360
 acnccntggt ggaracnaa rathgayccn ccngtnatga ayathacnaa rgtnaayggn 420
 wsnytnytn gtnathytna ygcncnaay ytnccntaym gntaycaraa rgaraaraay 480
 gtnwsnathg argaytayta ygarytnytn taymgngnt tyathathaa yaaywsnytn 540
 garaargarc araargnta ygarggngcn caymgngcng tngarathga rgcnynacn 600
 ccncaywsnw sntaytgygt ngtnngcngar athtaycarc cnatgytna ymgngnwsn 660
 armgngnwsn argarmgntg ygtngarath ccn 693

<210> 4
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker.

<400> 4
 Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 5
 <211> 699
 <212> DNA
 <213> Homo sapiens

<400> 5
 gagcccagat cttcagacaa aactcacaca tgcccaccgt gccacgacc tgaagccgag 60
 ggggcaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccg 120
 acccctgagg tcacatgctg ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
 ggcaaggagt acaagtcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc 360
 atctccaaaag ccaaagggca gcccgcagaa ccacaggtgt acaccctgcc cccatcccgg 420
 gatgagctga ccaagaacca ggtagcctg acctgcctgg tcaaaggctt ctatcccagc 480
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
 cccgtgctgg actccgacgg ctctctcttc ctctacagca agctcaccgt ggacaagagc 600
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
 tacacgcaga agagcctctc cctgtctccg ggtaaataa 699

<210> 6
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC29181

<400> 6
 gcggatccac tcagtcaacg catgagtctc tg 32

<210> 7
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC29182

<400> 7
 gcagatcttg gaatttcac acatctctct tca 33

<210> 8
 <211> 108
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(108)

<400> 8
 atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt ggc 48
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 1 5 10 15

gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc gag ttg aga cgc 96
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
 20 25 30

ttc cgt aga tcc 108

Phe Arg Arg Ser
35

<210> 9
<211> 36
<212> PRT
<213> Homo sapiens

<400> 9
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
20 25 30

Phe Arg Arg Ser
35

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Glu-Glu (CEE) Tag amino acid sequence

<400> 10
Glu Tyr Met Pro Met Glu
1 5

<210> 11
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> FLAG Tag amino acid sequence

<400> 11
Asp Tyr Lys Asp Asp Asp Lys
1 5

<210> 12
<211> 6
<212> PRT

001021.163260

<213> Artificial Sequence

<220>

<223> His Tag amino acid sequence

<400> 12

His His His His His His
1 5

<210> 13

<211> 210

<212> PRT

<213> Homo sapiens

<400> 13

Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln Arg Val Gln Phe Gln
1 5 10 15
Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln Pro Gly Arg Ala Leu
20 25 30
Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr Lys Ile Tyr Gly Gln
35 40 45
Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly Thr Gln Glu Leu Ser
50 55 60
Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln Glu Pro Tyr Tyr Gly
65 70 75 80
Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser Glu Trp Ser Met Thr
85 90 95
Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile Asp Pro Pro Val Met
100 105 110
Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val Ile Leu His Ala Pro
115 120 125
Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn Val Ser Ile Glu Asp
130 135 140
Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile Asn Asn Ser Leu Glu
145 150 155 160
Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg Ala Val Glu Ile Glu
165 170 175
Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val Ala Glu Ile Tyr Gln
180 185 190
Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu Glu Arg Cys Val Glu
195 200 205
Ile Pro
210

09728911.120100

<210> 14
 <211> 1116
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (21)...(557)

<400> 14

tcgagttaga attgtctgca atg gcc gcc ctg cag aaa tct gtg agc tct ttc	53
Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe	
1 5 10	
ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg	101
Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu	
15 20 25	
gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac	149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp	
30 35 40	
aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg	197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu	
45 50 55	
gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att	245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile	
60 65 70 75	
ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg	293
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu	
80 85 90	
atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa	341
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln	
95 100 105	
tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc	389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala	
110 115 120	

0970891.120100

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437
 Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
 125 130 135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485
 His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
 140 145 150 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533
 Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
 160 165 170

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac 587
 Met Ser Leu Arg Asn Ala Cys Ile
 175

taacccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca 647
 aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt 707
 tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag actttctaag 767
 catagatatt tattgataac atttcattgt aactggtgtt ctatacacag aaaacaattt 827
 attttttaaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa 887
 aaacccttaa atagcttcat gtttccataa tcagtacttt atatttataa atgtatttat 947
 tattattata agactgcatt ttatttatat cattttatta atatggattt atttatagaa 1007
 acatcattcg atattgctac ttgagtgtaa ggctaataat gatatttatg acaataatta 1067
 tagagctata acatgtttat ttgacctcaa taaacacttg gatatccta 1116

<210> 15

<211> 179

<212> PRT

<213> Homo sapiens

<400> 15

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 Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
 20 25 30
 Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
 35 40 45
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50 55 60
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 65 70 75 80

His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
 85 90 95
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
 100 105 110
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
 115 120 125
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
 130 135 140
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
 145 150 155 160
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
 165 170 175
 Ala Cys Ile

<210> 16

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC25963

<400> 16

agtcaacgca tgagtctctg aag

23

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28354

<400> 17

accaacaaag agccattgac ttg

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<210> 18

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC21195

<400> 18
gaggagacca taacccccga cag 23

<210> 19
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC21196

<400> 19
catagctccc accacacgat ttt 23

<210> 20
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC14063

<400> 20
caccagacat aatagctgac agact 25

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC17574

<400> 21
ggtrttgctc agcatgcaca c 21

<210> 22
<211> 24
<212> DNA
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<220>

<223> Oligonucleotide primer ZC17600

<400> 22

catgtaggcc atgaggtcca ccac

24

<210> 23

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC27659

<400> 23

tcaagctgag ttctctgtat gg

22

<210> 24

<211> 2831

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (34)...(1755)

<400> 24

tagaggccaa gggagggctc tgtgccagcc ccg atg agg acg ctg ctg acc atc
Met Arg Thr Leu Leu Thr Ile
1 5

54

ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
10 15 20

102

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
25 30 35

150

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile
40 45 50 55

198

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt

246

0973391.120100

Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys	
60 65 70	
cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac	294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn	
75 80 85	
ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc	342
Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly	
90 95 100	
cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act	390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr	
105 110 115	
acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att	438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile	
120 125 130 135	
cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc	486
Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly	
140 145 150	
cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta	534
His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu	
155 160 165	
gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag	582
Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln	
170 175 180	
aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc	630
Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly	
185 190 195	
acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac	678
Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr	
200 205 210 215	
atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc	726
Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe	
220 225 230	

tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc	774
Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys	
235 240 245	
tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc	822
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser	
250 255 260	
ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag	870
Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln	
265 270 275	
gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg	918
Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu	
280 285 290 295	
gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag	966
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu	
300 305 310	
ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta	1014
Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu	
315 320 325	
ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc	1062
Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro	
330 335 340	
cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc	1110
Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val	
345 350 355	
ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca	1158
Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro	
360 365 370 375	
ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc	1206
Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala	
380 385 390	
cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg	1254
Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met	
395 400 405	

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 Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys
 410 415 420

cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc 1350
 His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser
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tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg 1398
 Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met
 440 445 450 455

gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc 1446
 Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys
 460 465 470

aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg 1494
 Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly
 475 480 485

aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag 1542
 Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln
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 Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro
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 Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser
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 Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser
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gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc 1734
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Met	His	Leu	Gly	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr
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 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
 485 490 495
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 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
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 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
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	50					55					60				
Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr
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Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro
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 Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr
 85 90 95
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 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
 115 120 125
 Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
 130 135 140
 His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
 145 150 155 160
 Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
 165 170 175
 Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
 180 185 190
 Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
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 Thr Arg Gln
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